Sequence Range: 1 to 1689

```
                10          20          30          40
AAT CCT TTT CCT GGC ACC TCT GAT ATC CTT TTG AAA TTC ATC TTA AAG

50          60          70          80          90
AAT CCC TAG GCT GCT ATC ACA TGT GGC ATC TTT GTT GAG TAC ATG AAT

  100         110         120         130         140
AAA TCA ACT GGT GTG TTT TAC GAA GGA TGA TTA TGC TTC ATT GTG GGA

    150         160         170         180         190
TTG TAT TTT TCT TCT TCT ATC ACA GGG AGA AGT GAA ATG ACA ACC TCA
                                                Met Thr Thr Ser>

        200         210         220         230         240
CTA GAT ACA GTT GAG ACC TTT GGT ACC ACA TCC TAC TAT GAT GAC GTG
Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr Tyr Asp Asp Val>

            250         260         270         280
GGC CTG CTC TGT GAA AAA GCT GAT ACC AGA GCA CTG ATG GCC CAG TTT
Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe>

290         300         310         320         330
GTG CCC CCG CTG TAC TCC CTG GTG TTC ACT GTG GGC CTC TTG GGC AAT
Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn>

  340         350         360         370         380
GTC GTG GTG GTG ATG ATC CTC ATA AAA TAC AGG AGG CTC CGA ATT ATG
Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met>

    390         400         410         420         430
ACC AAC ATC TAC CTG CTC AAC CTG GCC ATT TCG GAC CTG CTC TTC CTC
Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu>

        440         450         460         470         480
GTC ACC CTT CCA TTC TGG ATC CAC TAT GTC AGG GGC CAT AAC TGG GTT
Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly His Asn Trp Val>

            490         500         510         520
TTT GGC CAT GGC ATG TGT AAG CTC CTC TCA GGG TTT TAT CAC ACA GGC
Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe Tyr His Thr Gly>

530         540         550         560         570
TTG TAC AGC GAG ATC TTT TTC ATA ATC CTG CTG ACA ATC GAC AGG TAC
Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr>

  580         590         600         610         620
CTG GCC ATT GTC CAT GCT GTG TTT GCC CTT CGA GCC CGG ACT GTC ACT
```

FIGURE 1A

Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr>

630 640 650 660 670

TTT GGT GTC ATC ACC AGC ATC GTC ACC TGG GGC CTG GCA GTG CTA GCA
Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu Ala Val Leu Ala>

680 690 700 710 720

GCT CTT CCT GAA TTT ATC TTC TAT GAG ACT GAA GAG TTG TTT GAA GAG
Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu Leu Phe Glu Glu>

730 740 750 760

ACT CTT TGC AGT GCT CTT TAC CCA GAG GAT ACA GTA TAT AGC TGG AGG
Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val Tyr Ser Trp Arg>

770 780 790 800 810

CAT TTC CAC ACT CTG AGA ATG ACC ATC TTC TGT CTC GTT CTC CCT CTG
His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu Val Leu Pro Leu>

820 830 840 850 860

CTC GTT ATG GCC ATC TGC TAC ACA GGA ATC ATC AAA ACG CTG CTG AGG
Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys Thr Leu Leu Arg>

870 880 890 900 910

TGC CCC AGT AAA AAA AAG TAC AAG GCC ATC CGG CTC ATT TTT GTC ATC
Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu Ile Phe Val Ile>

920 930 940 950 960

ATG GCG GTG TTT TTC ATT TTC TGG ACA CCC TAC AAT GTG GCT ATC CTT
Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn Val Ala Ile Leu>

970 980 990 1000

CTC TCT TCC TAT CAA TCC ATC TTA TTT GGA AAT GAC TGT GAG CGG ACG
Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp Cys Glu Arg Thr>

1010 1020 1030 1040 1050

AAG CAT CTG GAC CTG GTC ATG CTG GTG ACA GAG GTG ATC GCC TAC TCC
Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val Ile Ala Tyr Ser>

1060 1070 1080 1090 1100

CAC TGC TGC ATG AAC CCG GTG ATC TAC GCC TTT GTT GGA GAG AGG TTC
His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val Gly Glu Arg Phe>

1110 1120 1130 1140 1150

CGG AAG TAC CTG CGC CAC TTC TTC CAC AGG CAC TTG CTC ATG CAC CTG
Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu Leu Met His Leu>

1160 1170 1180 1190 1200

GGC AGA TAC ATC CCA TTC CTT CCT AGT GAG AAG CTG GAA AGA ACC AGC
Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu Glu Arg Thr Ser>

FIGURE 1B

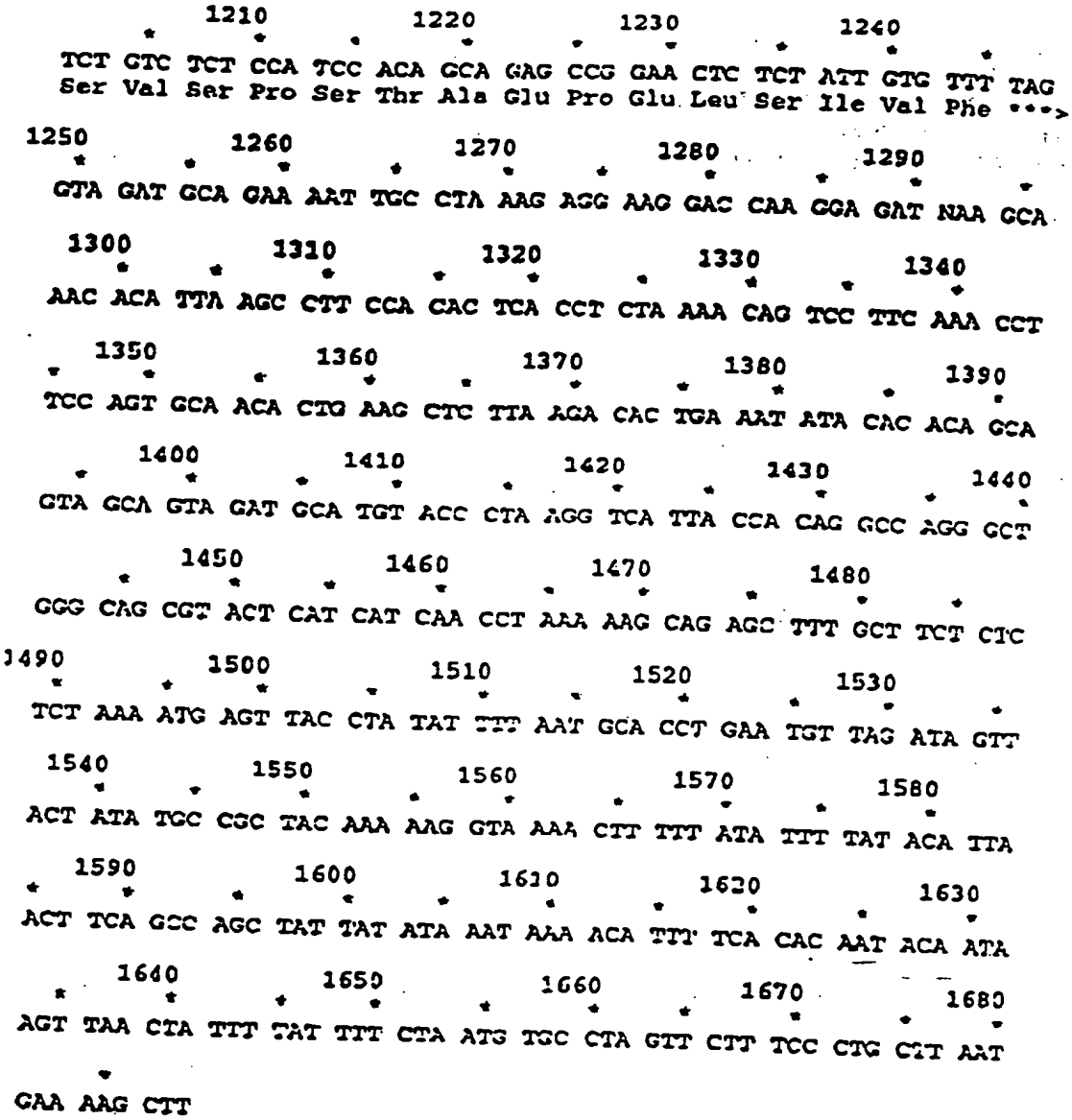

1210
1220
1230
1240
TCT GTC TCT CCA TCC ACA GCA GAG CCG GAA CTC TCT ATT GTG TTT TAG
Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser Ile Val Phe ***>
1250
1260
1270
1280
1290
GTA GAT GCA GAA AAT TGC CTA AAG AGG AAG GAC CAA CGA GAT NAA GCA
1300
1310
1320
1330
1340
AAC ACA TTA AGC CTT CCA CAC TCA CCT CTA AAA CAG TCC TTC AAA CCT
1350
1360
1370
1380
1390
TCC AGT GCA ACA CTG AAG CTC TTA AGA CAC TGA AAT ATA CAC ACA GCA
1400
1410
1420
1430
1440
GTA GCA GTA GAT GCA TGT ACC CTA AGG TCA TTA CCA CAG GCC AGG GCT
1450
1460
1470
1480
GGG CAG CGT ACT CAT CAT CAA CCT AAA AAG CAG AGC TTT GCT TCT CTC
1490
1500
1510
1520
1530
TCT AAA ATG AGT TAC CTA TAT TTT AAT GCA CCT GAA TGT TAG ATA GTT
1540
1550
1560
1570
1580
ACT ATA TGC CGC TAC AAA AAG GTA AAA CTT TTT ATA TTT TAT ACA TTA
1590
1600
1610
1620
1630
ACT TCA GCC AGC TAT TAT ATA AAT AAA ACA TTT TCA CAC AAT ACA ATA
1640
1650
1660
1670
1680
AGT TAA CTA TTT TAT TTT CTA ATG TGC CTA GTT CTT TCC CTG CTT AAT
GAA AAG CTT

FIGURE 1C

```
                10         20         30         40         50         60
TTGTGCTTAT CCGGGCAAGA ACTTATCGAA ATACAATAGA AGACCCACGC GTCCGGTTTT

                70         80         90        100        110
TACTTAGAAG AGATTTTCAG GGAGAAGTGA A ATG ACA ACC TCA CTA GAT ACA GTT
                                   M   T   T   S   L   D   T   V>

    120          130          140          150          160
GAG ACC TTT GGT ACC ACA TCC TAC TAT GAT GAC GTG GGC CTG CTC TGT
 E   T   F   G   T   T   S   Y   Y   D   D   V   G   L   L   C>

    170          180          190          200          210
GAA AAA GCT GAT ACC AGA GCA CTG ATG GCC CAG TTT GTG CCC CCG CTG
 E   K   A   D   T   R   A   L   M   A   Q   F   V   P   P   L>

    220          230          240          250
TAC TCC CTG GTG TTC ACT GTG GGC CTC TTG GGC AAT GTG GTG GTG GTG
 Y   S   L   V   F   T   V   G   L   L   G   N   V   V   V   V>

260          270          280          290          300
ATG ATC CTC ATA AAA TAC AGG AGG CTC CGA ATT ATG ACC AAC ATC TAC
 M   I   L   I   K   Y   R   R   L   R   I   M   T   N   I   Y>

310          320          330          340          350
CTG CTC AAC CTG GCC ATT TCG GAC CTG CTC TTC CTC GTC ACC CTT CCA
 L   L   N   L   A   I   S   D   L   L   F   L   V   T   L   P>

    360          370          380          390          400
TTC TGG ATC CAC TAT GTC AGG GGG CAT AAC TGG GTT TTT GGC CAT GGC
 F   W   I   H   Y   V   R   G   H   N   W   V   F   G   H   G>

    410          420          430          440          450
ATG TGT AAG CTC CTC TCA GGG TTT TAT CAC ACA GGC TTG TAC AGC GAG
 M   C   K   L   L   S   G   F   Y   H   T   G   L   Y   S   E>

    460          470          480          490
ATC TTT TTC ATA ATC CTG CTG ACA ATC GAC AGG TAC CTG GCC ATT GTC
 I   F   F   I   I   L   L   T   I   D   R   Y   L   A   I   V>

500          510          520          530          540
CAT GCT GTG TTT GCC CTT CGA GCC CGG ACT GTC ACT TTT GGT GTC ATC
 H   A   V   F   A   L   R   A   R   T   V   T   F   G   V   I>

550          560          570          580          590
ACC AGC ATC GTC ACC TGG GGC CTG GCA GTG CTA GCA GCT CTT CCT GAA
 T   S   I   V   T   W   G   L   A   V   L   A   A   L   P   E>
```

FIGURE 2A

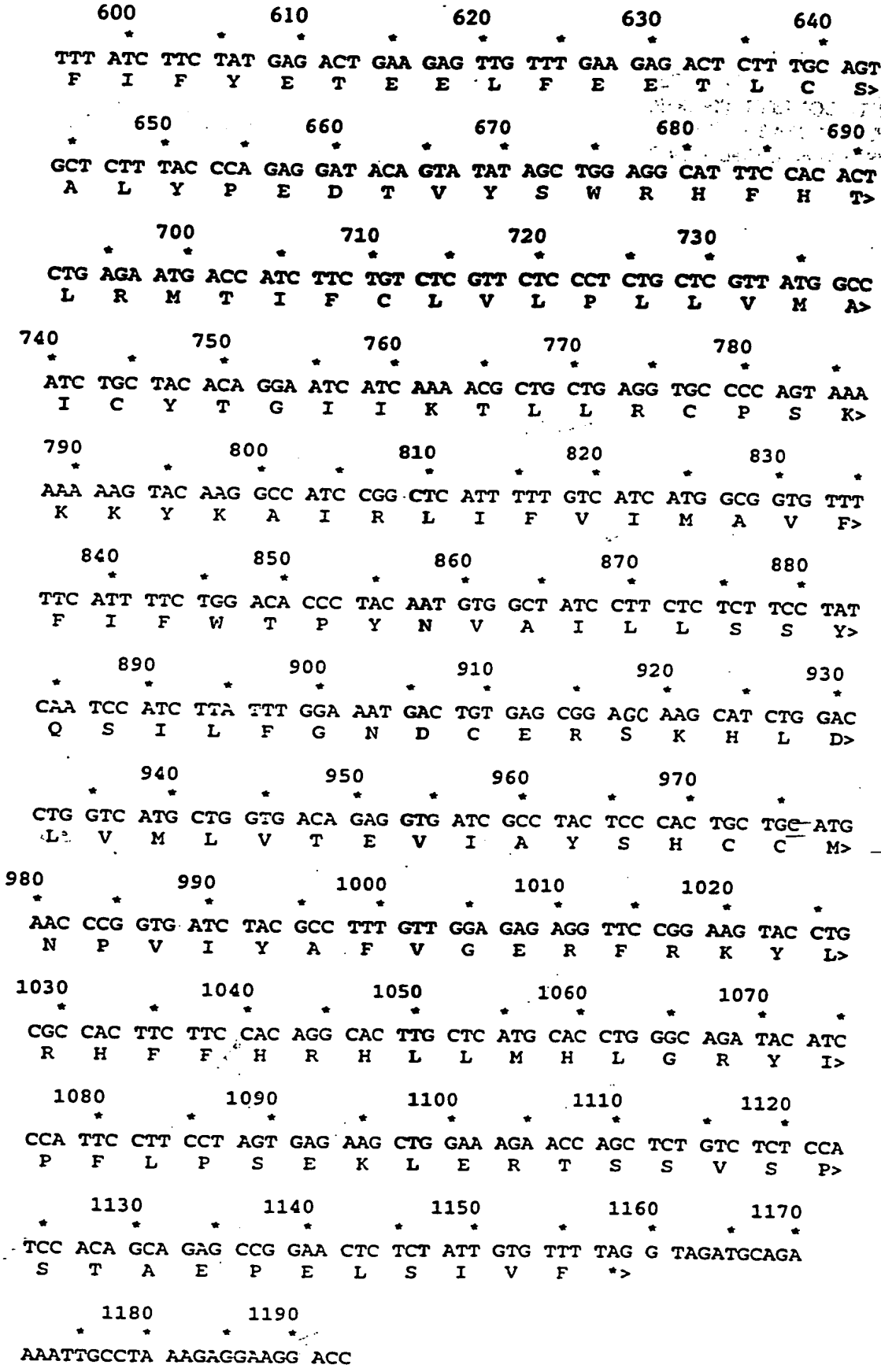

600 610 620 630 640
TTT ATC TTC TAT GAG ACT GAA GAG TTG TTT GAA GAG ACT CTT TGC AGT
F I F Y E T E E L F E E T L C S>
650 660 670 680 690
GCT CTT TAC CCA GAG GAT ACA GTA TAT AGC TGG AGG CAT TTC CAC ACT
A L Y P E D T V Y S W R H F H T>
700 710 720 730
CTG AGA ATG ACC ATC TTC TGT CTC GTT CTC CCT CTG CTC GTT ATG GCC
L R M T I F C L V L P L L V M A>
740 750 760 770 780
ATC TGC TAC ACA GGA ATC ATC AAA ACG CTG CTG AGG TGC CCC AGT AAA
I C Y T G I I K T L L R C P S K>
790 800 810 820 830
AAA AAG TAC AAG GCC ATC CGG CTC ATT TTT GTC ATC ATG GCG GTG TTT
K K Y K A I R L I F V I M A V F>
840 850 860 870 880
TTC ATT TTC TGG ACA CCC TAC AAT GTG GCT ATC CTT CTC TCT TCC TAT
F I F W T P Y N V A I L L S S Y>
890 900 910 920 930
CAA TCC ATC TTA TTT GGA AAT GAC TGT GAG CGG AGC AAG CAT CTG GAC
Q S I L F G N D C E R S K H L D>
940 950 960 970
CTG GTC ATG CTG GTG ACA GAG GTG ATC GCC TAC TCC CAC TGC TGC ATG
L V M L V T E V I A Y S H C C M>
980 990 1000 1010 1020
AAC CCG GTG ATC TAC GCC TTT GTT GGA GAG AGG TTC CGG AAG TAC CTG
N P V I Y A F V G E R F R K Y L>
1030 1040 1050 1060 1070
CGC CAC TTC TTC CAC AGG CAC TTG CTC ATG CAC CTG GGC AGA TAC ATC
R H F F H R H L L M H L G R Y I>
1080 1090 1100 1110 1120
CCA TTC CTT CCT AGT GAG AAG CTG GAA AGA ACC AGC TCT GTC TCT CCA
P F L P S E K L E R T S S V S P>
1130 1140 1150 1160 1170
TCC ACA GCA GAG CCG GAA CTC TCT ATT GTG TTT TAG G TAGATGCAGA
S T A E P E L S I V F *>
1180 1190
AAATTGCCTA AAGAGGAAGG ACC

FIGURE 2B

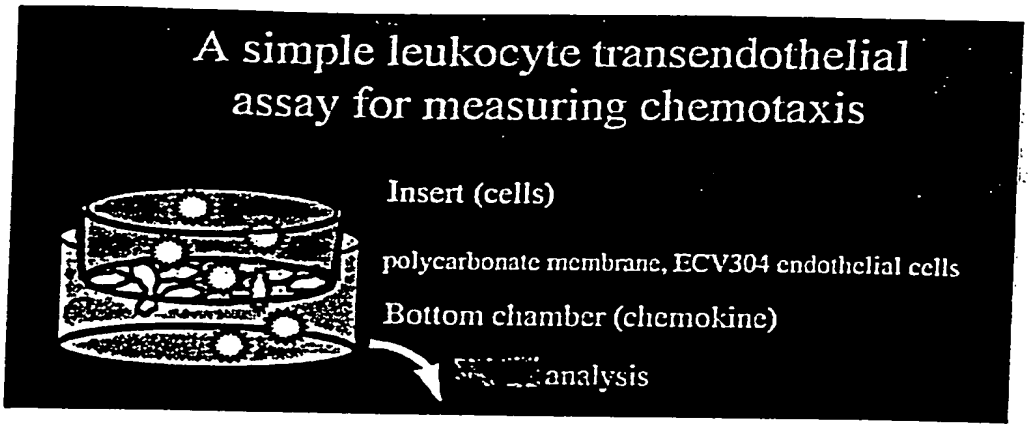


FIGURE 3

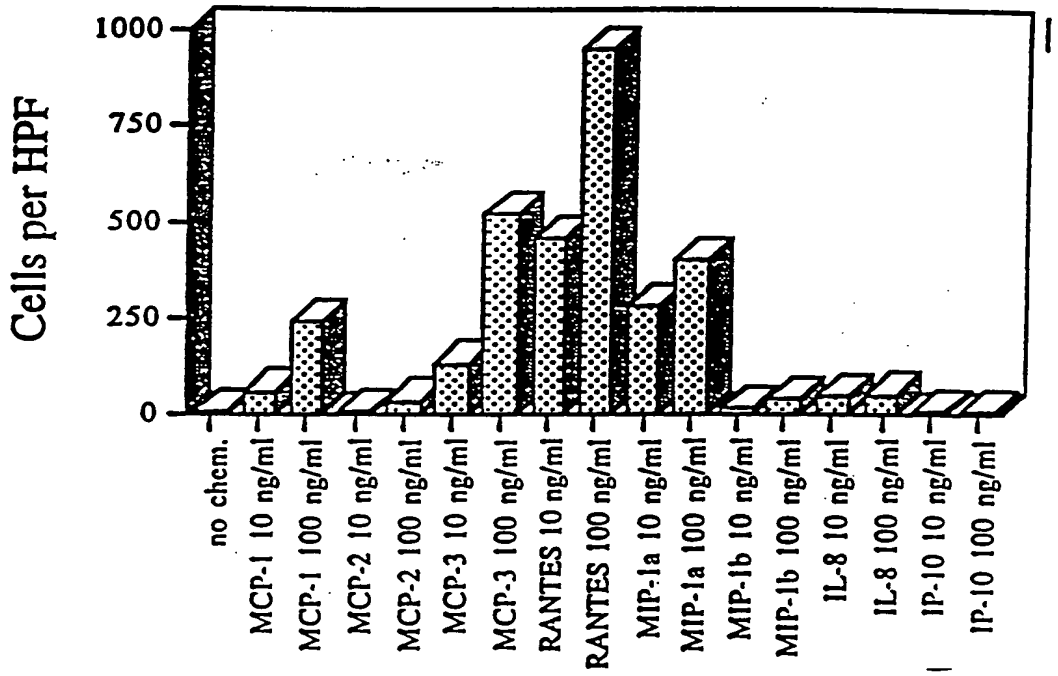

Cells per HPF
1000
750
500
250
0
no chem.
MCP-1 10 ng/ml
MCP-1 100 ng/ml
MCP-2 10 ng/ml
MCP-2 100 ng/ml
MCP-3 10 ng/ml
MCP-3 100 ng/ml
RANTES 10 ng/ml
RANTES 100 ng/ml
MIP-1a 10 ng/ml
MIP-1a 100 ng/ml
MIP-1b 10 ng/ml
MIP-1b 100 ng/ml
IL-8 10 ng/ml
IL-8 100 ng/ml
IP-10 10 ng/ml
IP-10 100 ng/ml

FIGURE 4

Expression of Eos L2 on stably transfected L1-2 cells

Flag staining of different clones

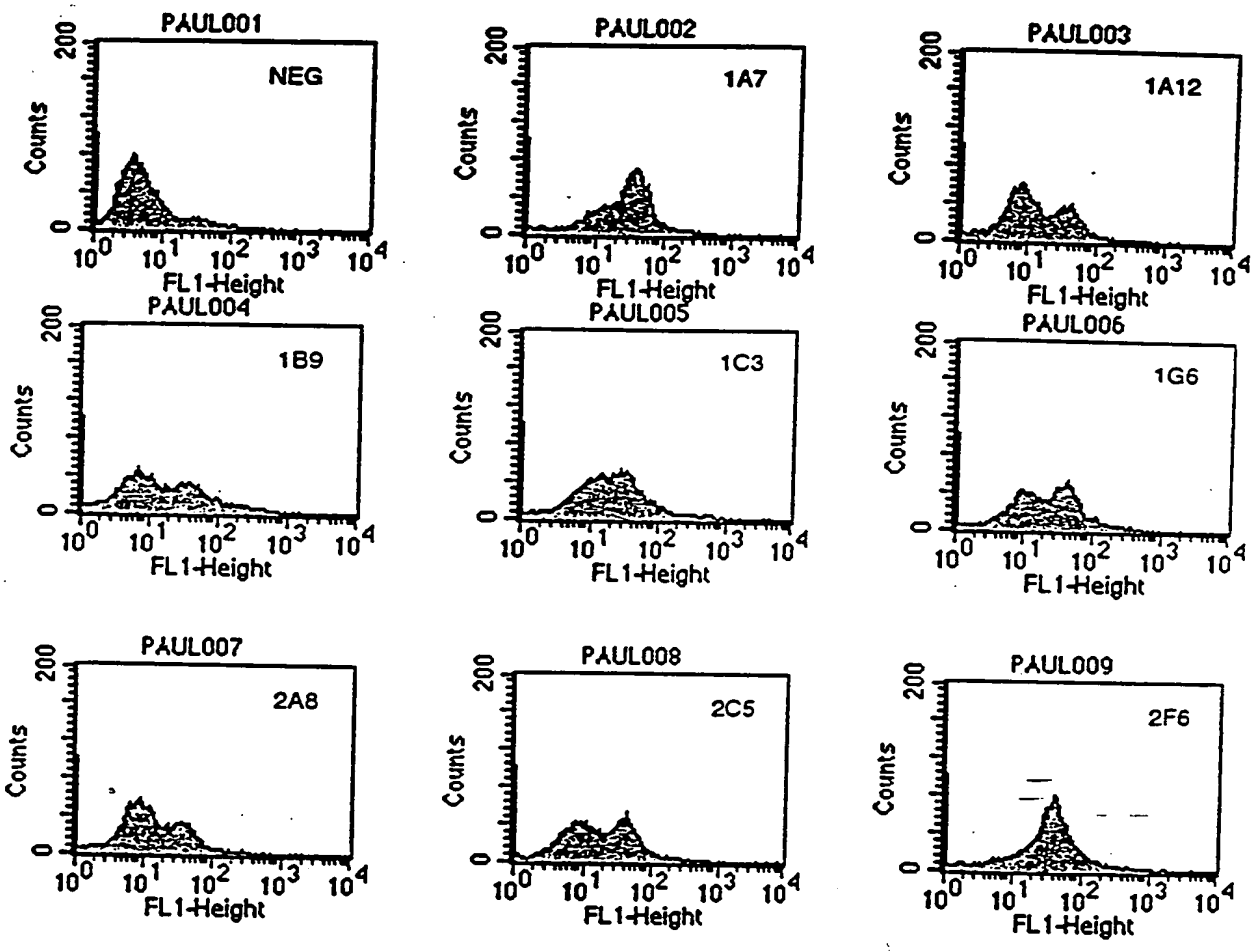


FIGURE 5

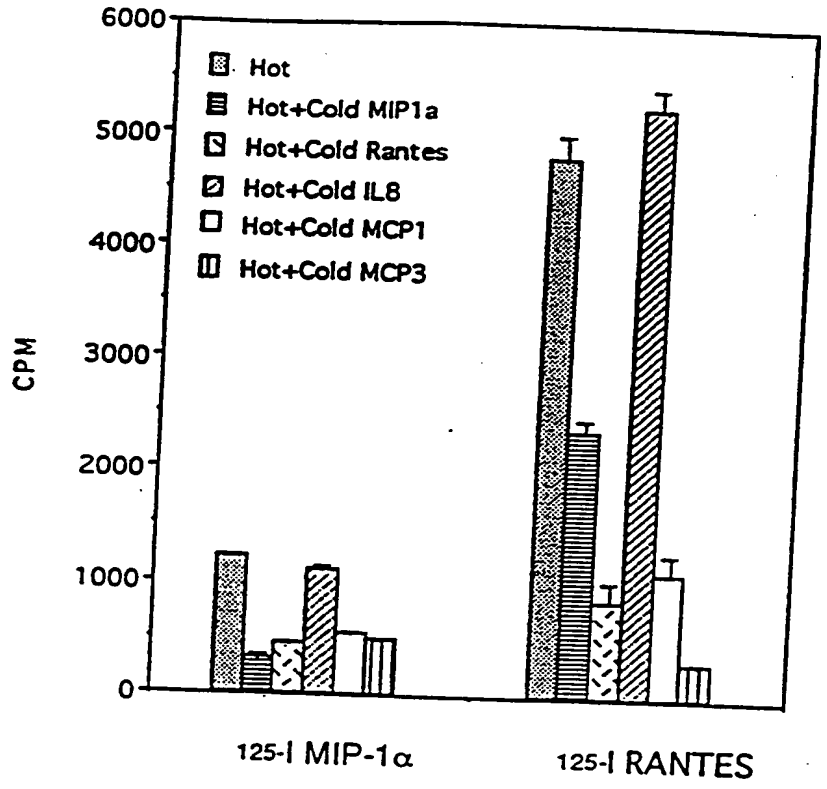

6000
5000
4000
3000
2000
1000
0
CPM
Hot
Hot+Cold MIP1a
Hot+Cold Rantes
Hot+Cold IL8
Hot+Cold MCP1
Hot+Cold MCP3
125-I MIP-1α
125-I RANTES

FIGURE 6

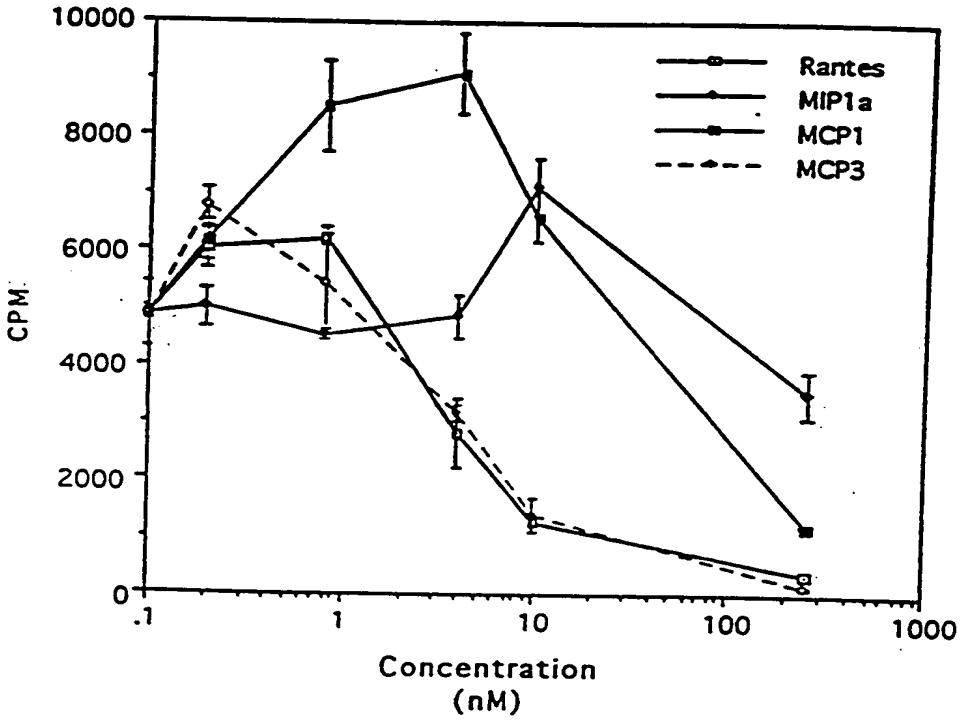

10000
8000
6000
4000
2000
0
CPM
.1
1
10
100
1000
Concentration
(nM)
Rantes
MIP1a
MCP1
MCP3

FIGURE 7

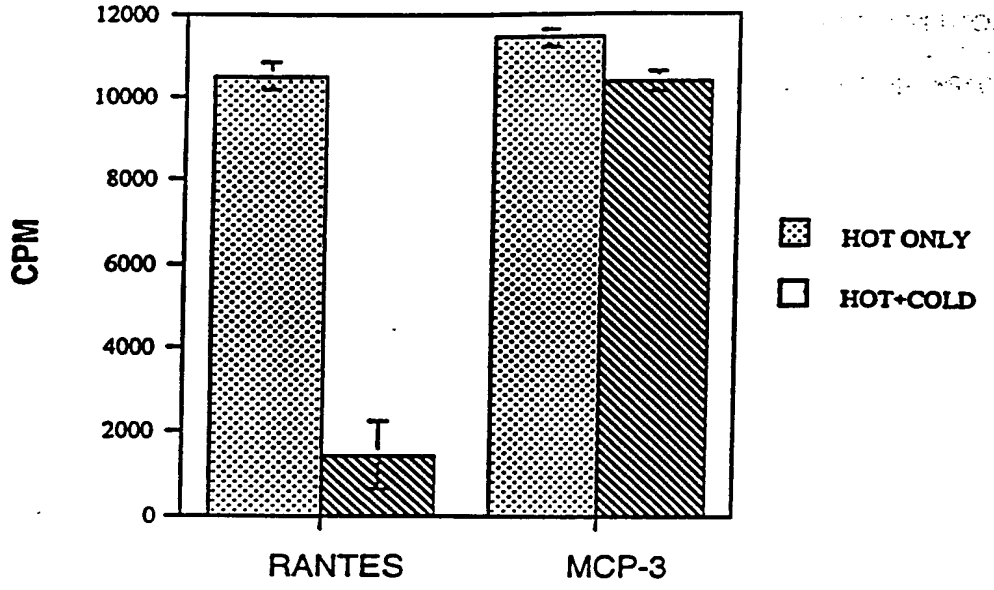

12000
10000
8000
6000
4000
2000
0
CPM
RANTES
MCP-3
HOT ONLY
HOT+COLD

FIGURE 8

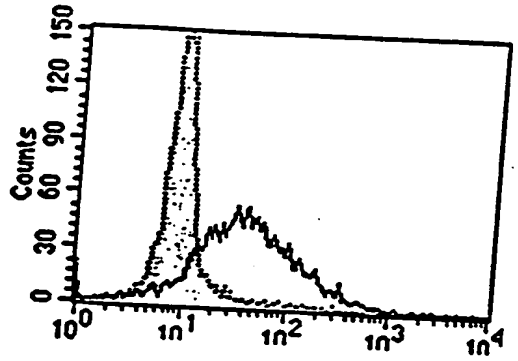


FIGURE 9A

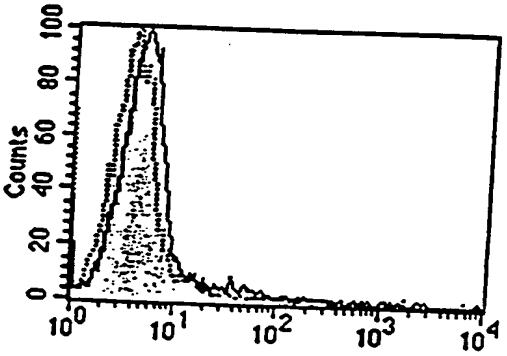


FIGURE 9B

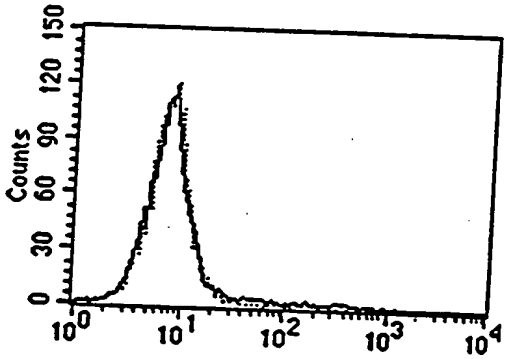


FIGURE 9C

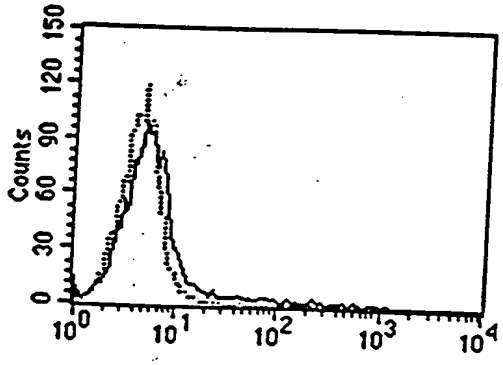


FIGURE 9D

Fluorescence intensity →

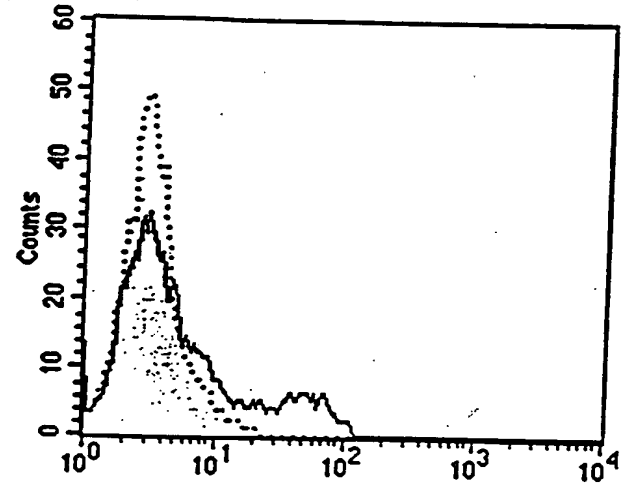


FIGURE 10A

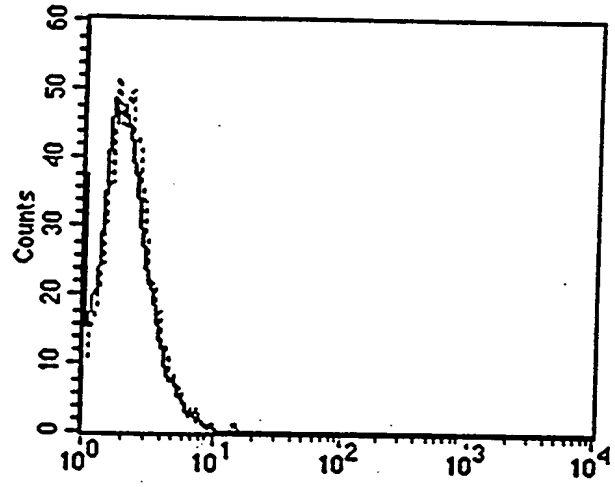


FIGURE 10B

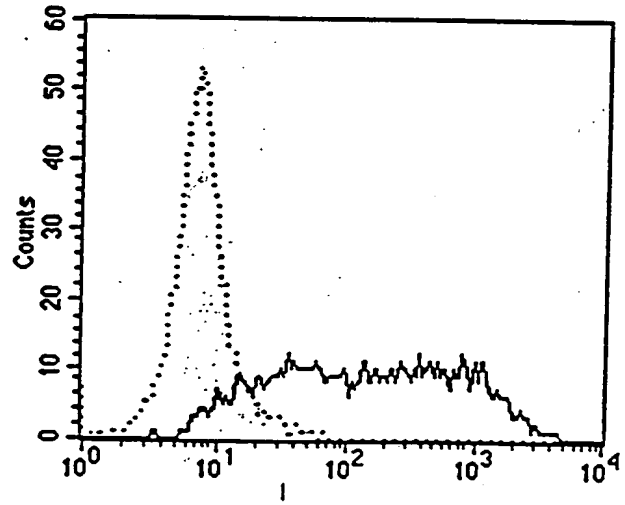


FIGURE 10C

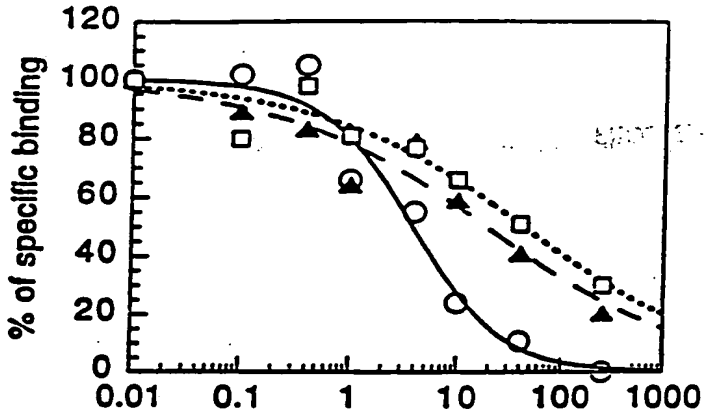


FIGURE 11A

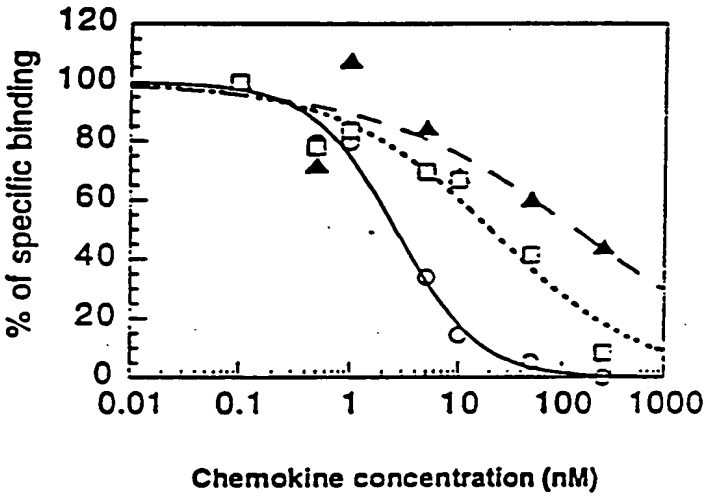


FIGURE 11B

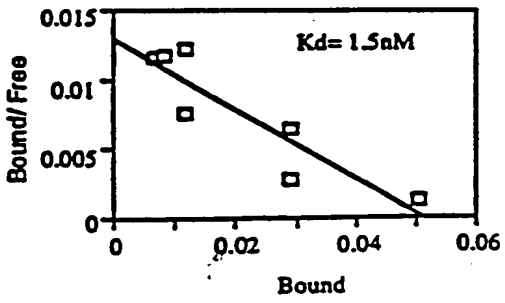


FIGURE 11C

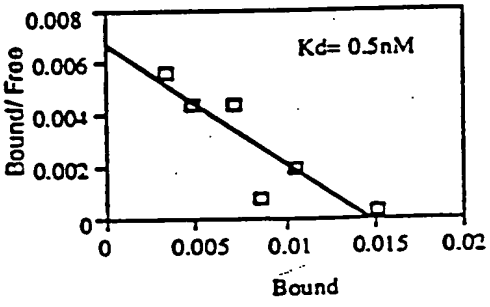


FIGURE 11D

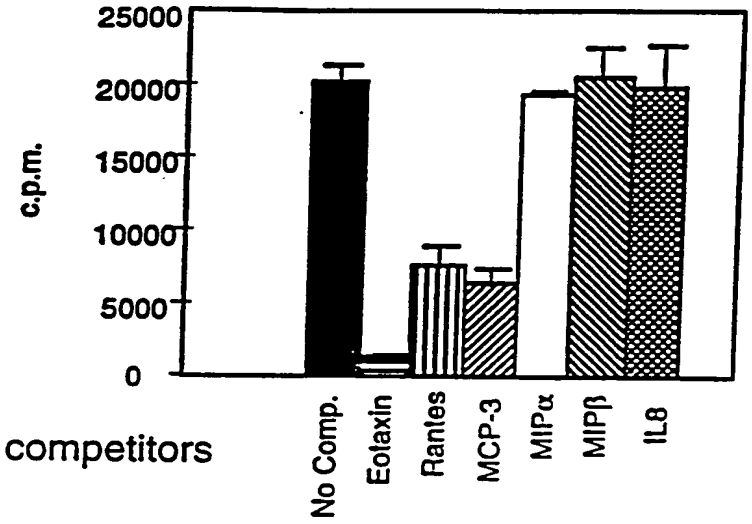

25000
20000
15000
10000
5000
0
c.p.m.
competitors
No Comp.
Eotaxin
Rantes
MCP-3
MIPα
MIPβ
IL8

FIGURE 12

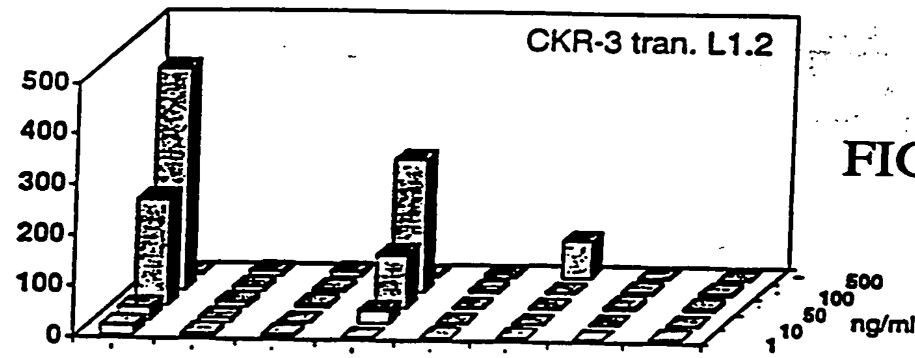


FIGURE 13A

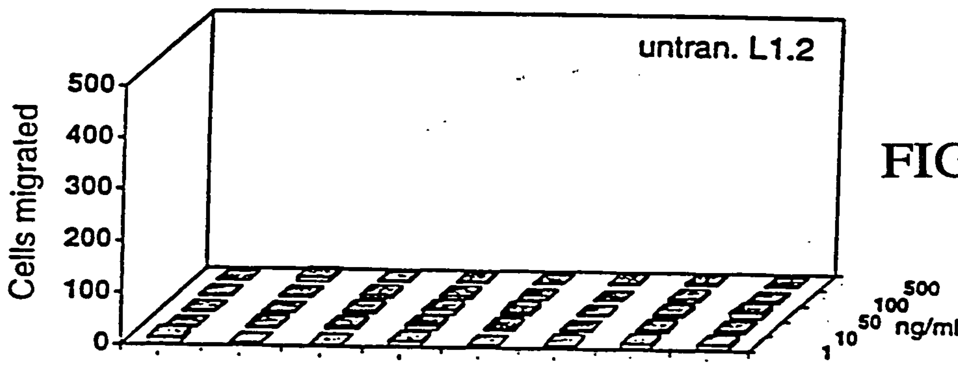


FIGURE 13B

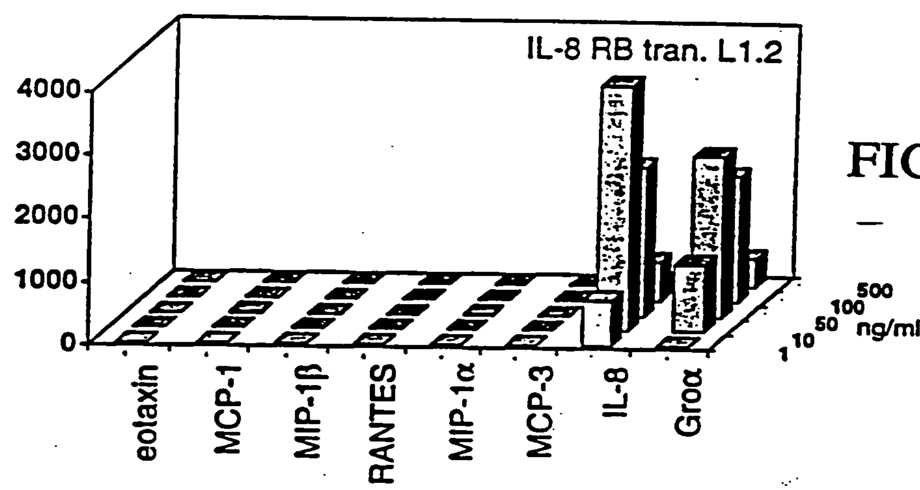


FIGURE 13C

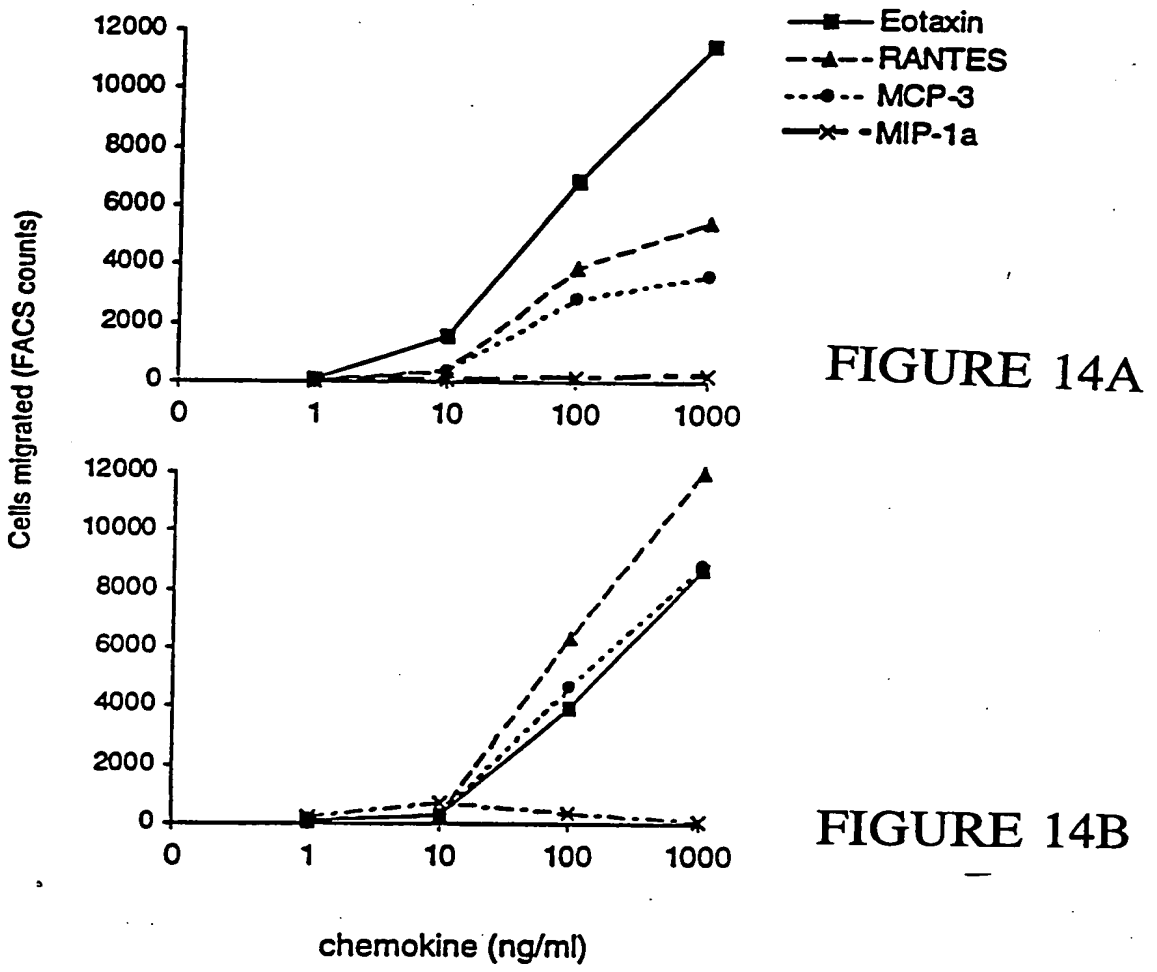


FIGURE 14A

FIGURE 14B

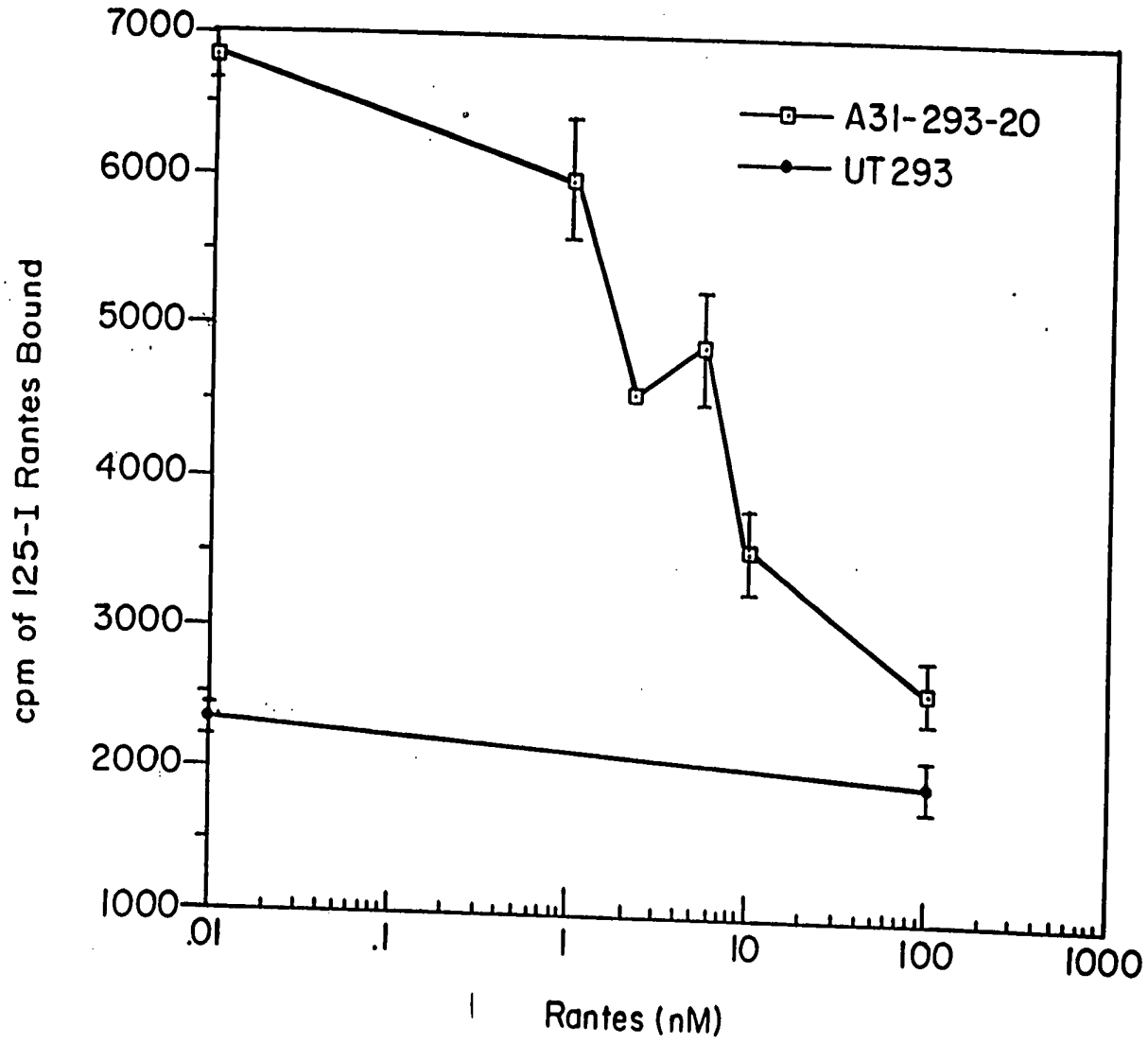


FIGURE 15

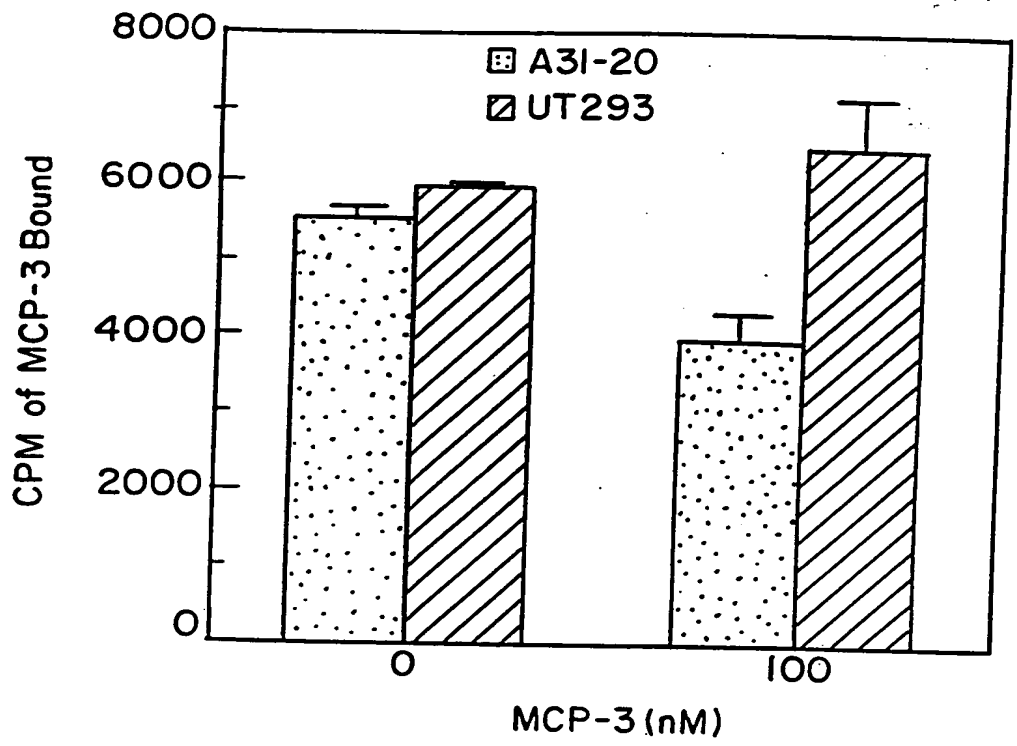


FIGURE 16

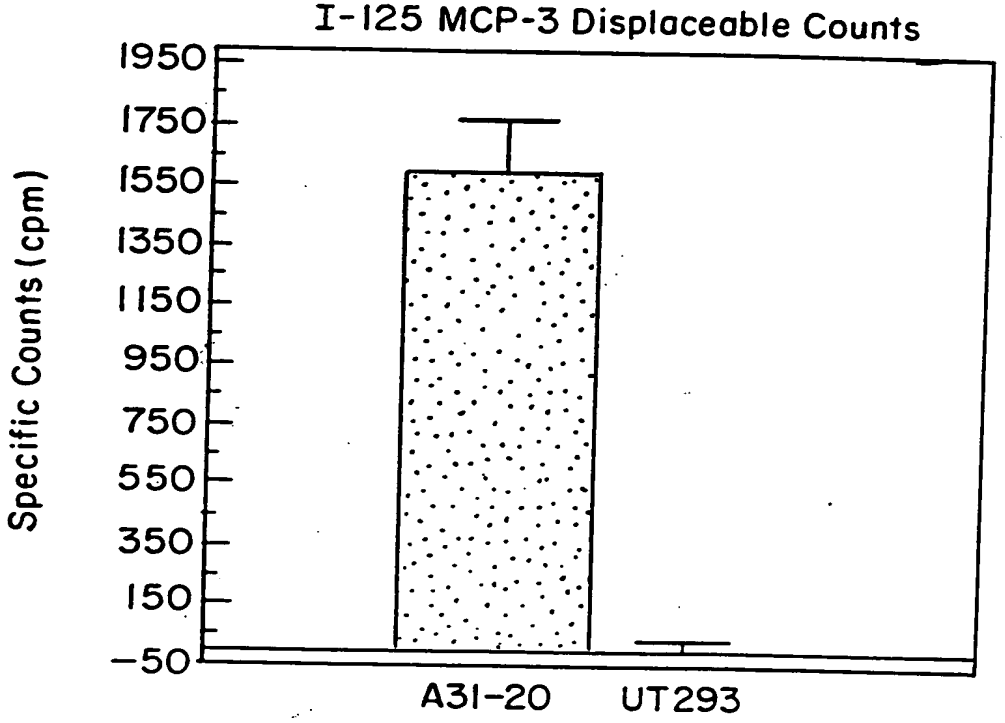
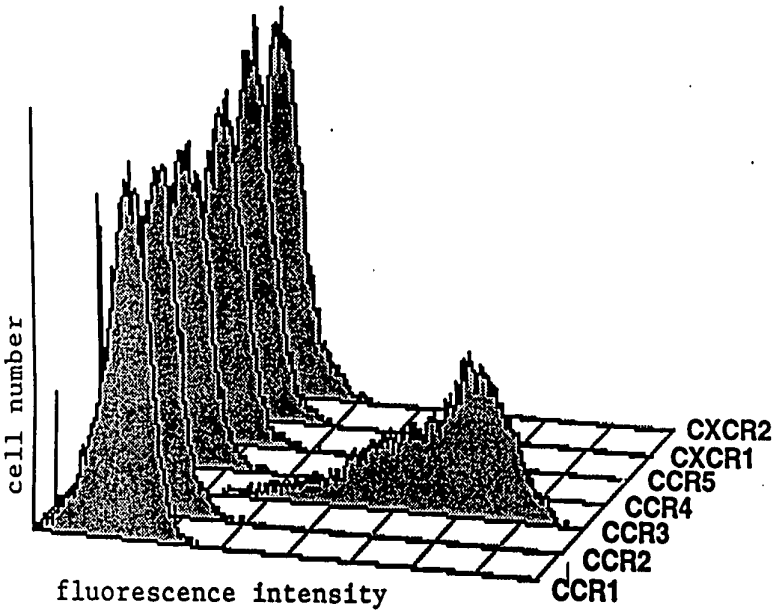


FIGURE 17

7B11: a monoclonal antibody that specifically recognizes CCR3 and stains eosinophils

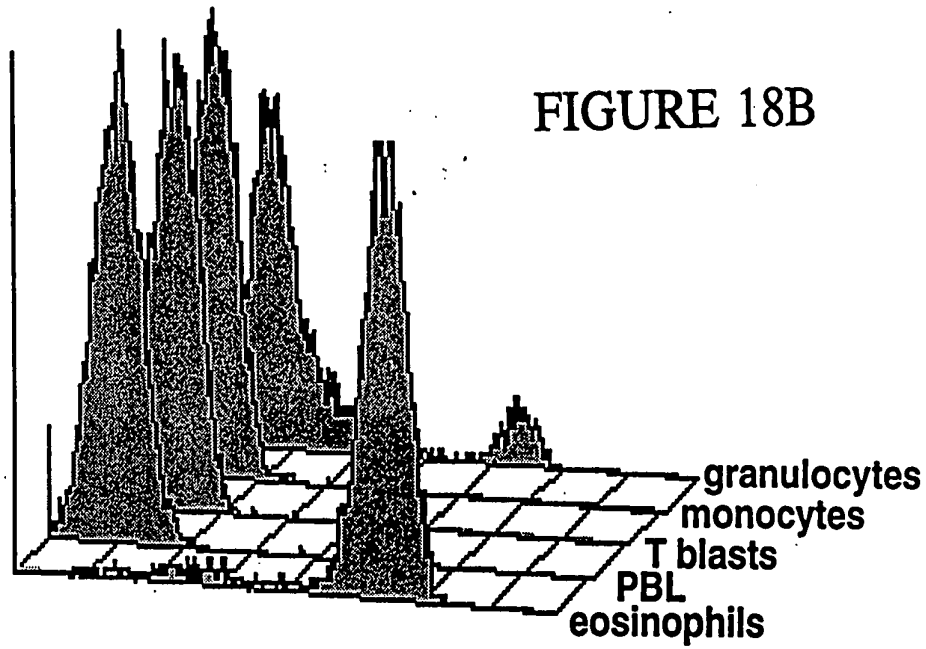
L1.2 Transfectants

FIGURE 18A



Leukocytes

FIGURE 18B



Fluorescence intensity 7B11 ⟶

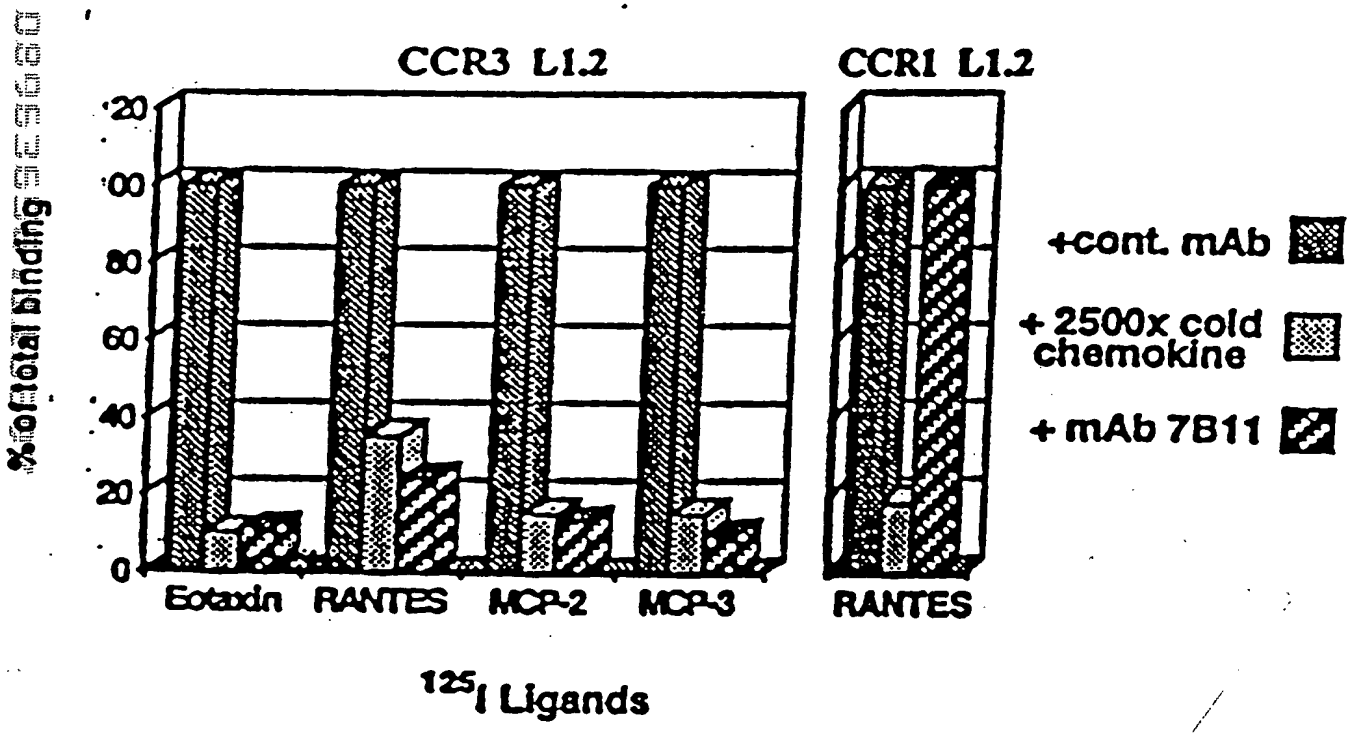

CCR3 L1.2
CCR1 L1.2
% Total Binding
0
20
40
60
80
100
Eotaxin
RANTES
MCP-2
MCP-3
RANTES
+cont. mAb
+ 2500x cold chemokine
+ mAb 7B11
125I Ligands

FIGURE 18C

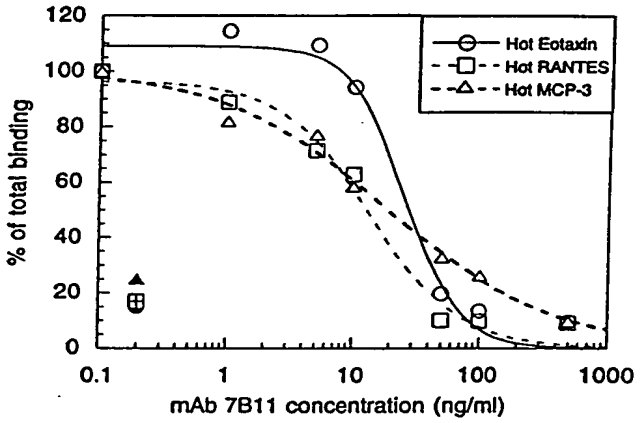

120
100
80
60
40
20
0
% of total binding
0.1
1
10
100
1000
mAb 7B11 concentration (ng/ml)
Hot Eotaxin
Hot RANTES
Hot MCP-3

FIGURE 19

Inhibition of eosinophil chemotaxis to CC chemokines by mAb 7B11

FIGURE 20A **eotaxin migration**

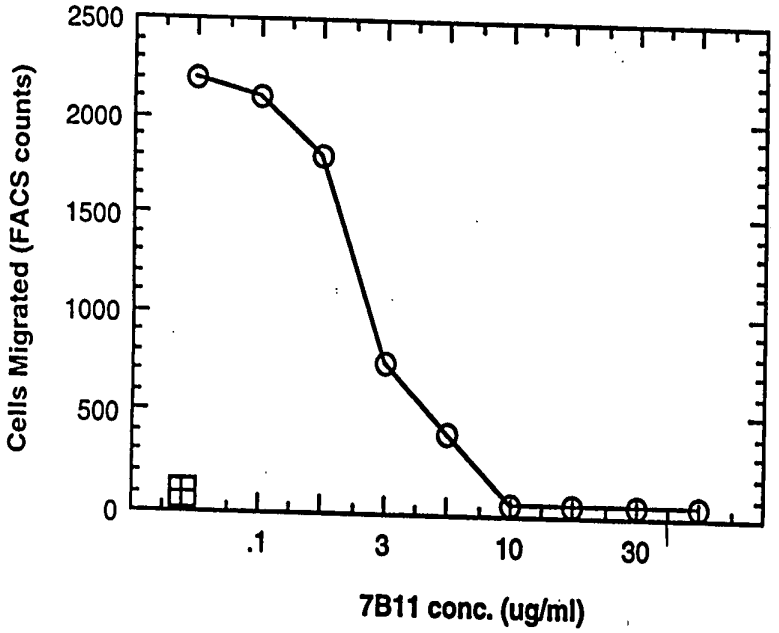
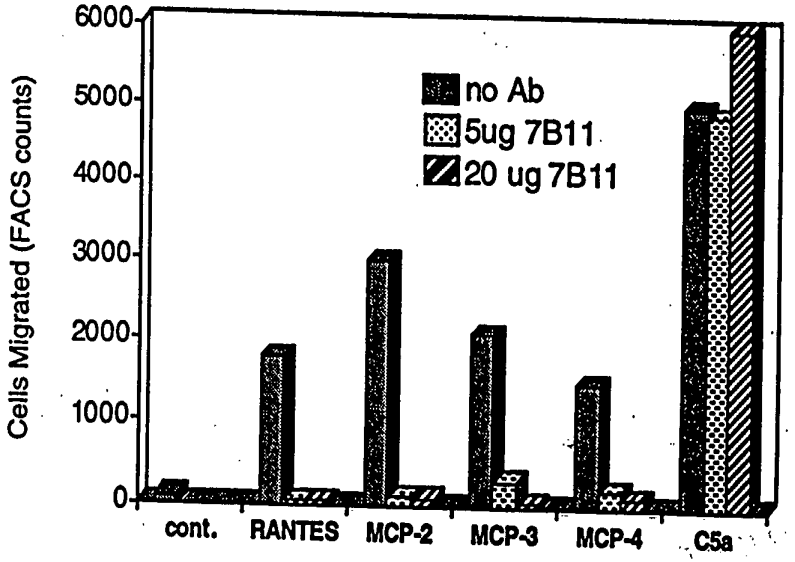


FIGURE 20B **other eos. chemoattractants**



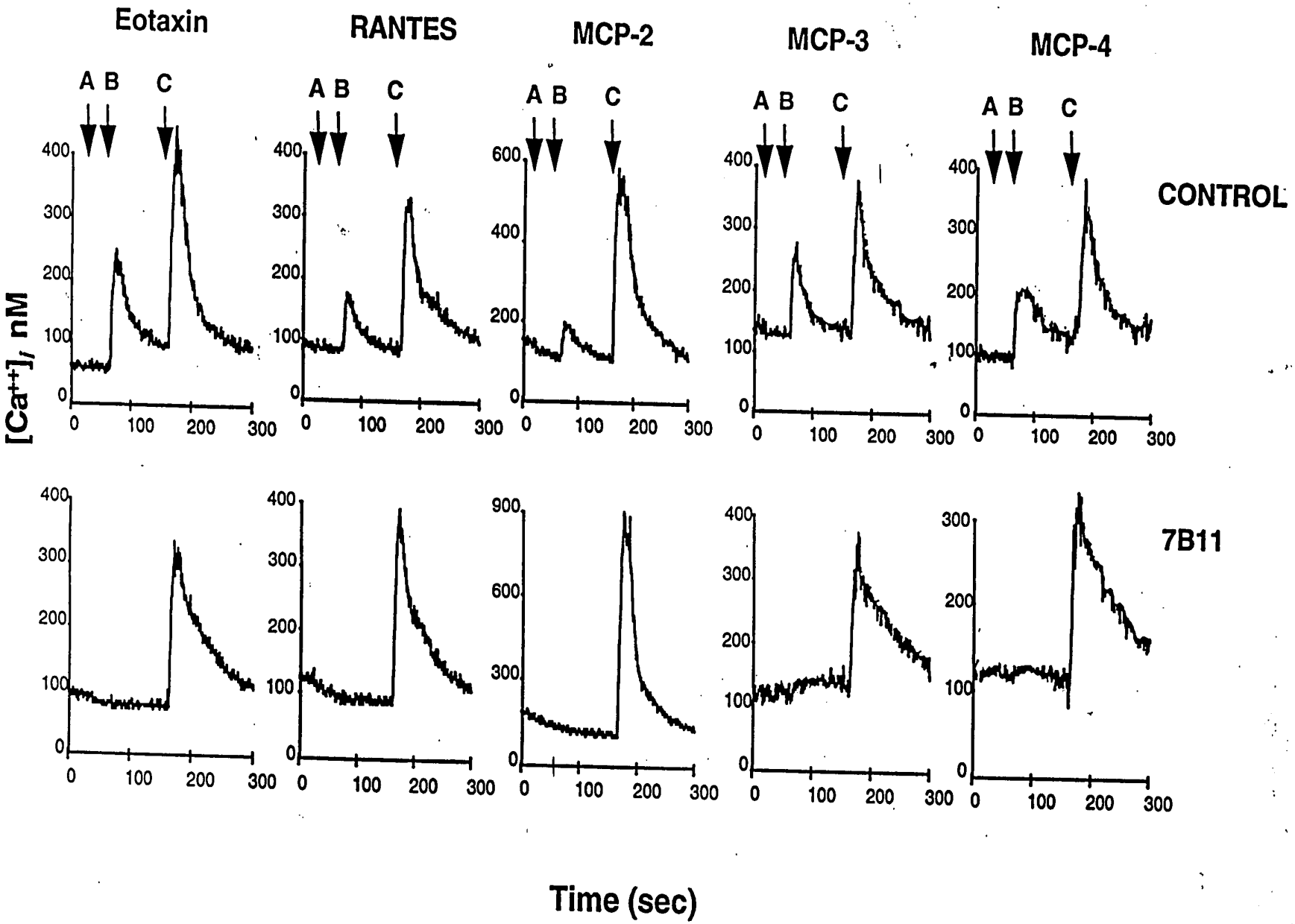


FIGURE 21

FIGURE 22A

FIGURE 22B

FIGURE 22C

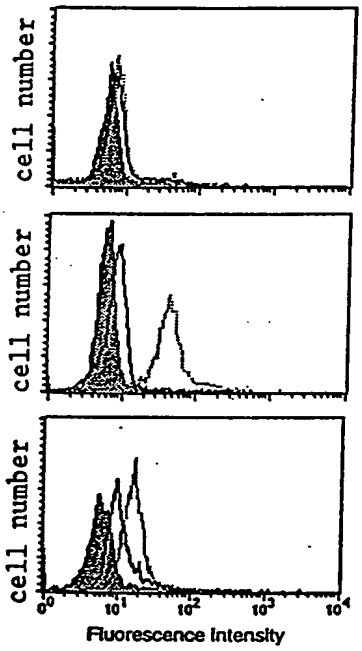


FIGURE 22D

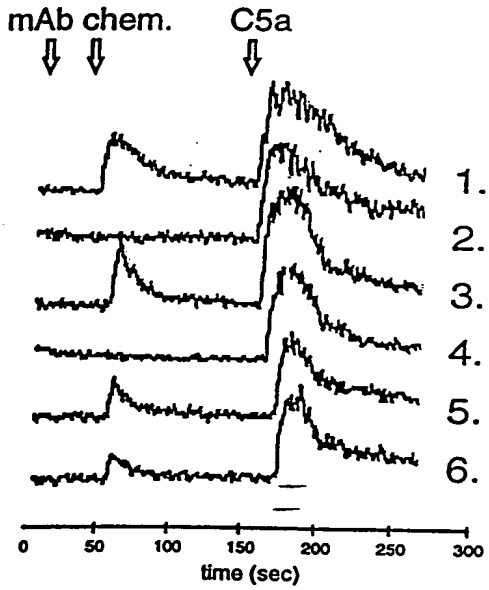


FIGURE 23A

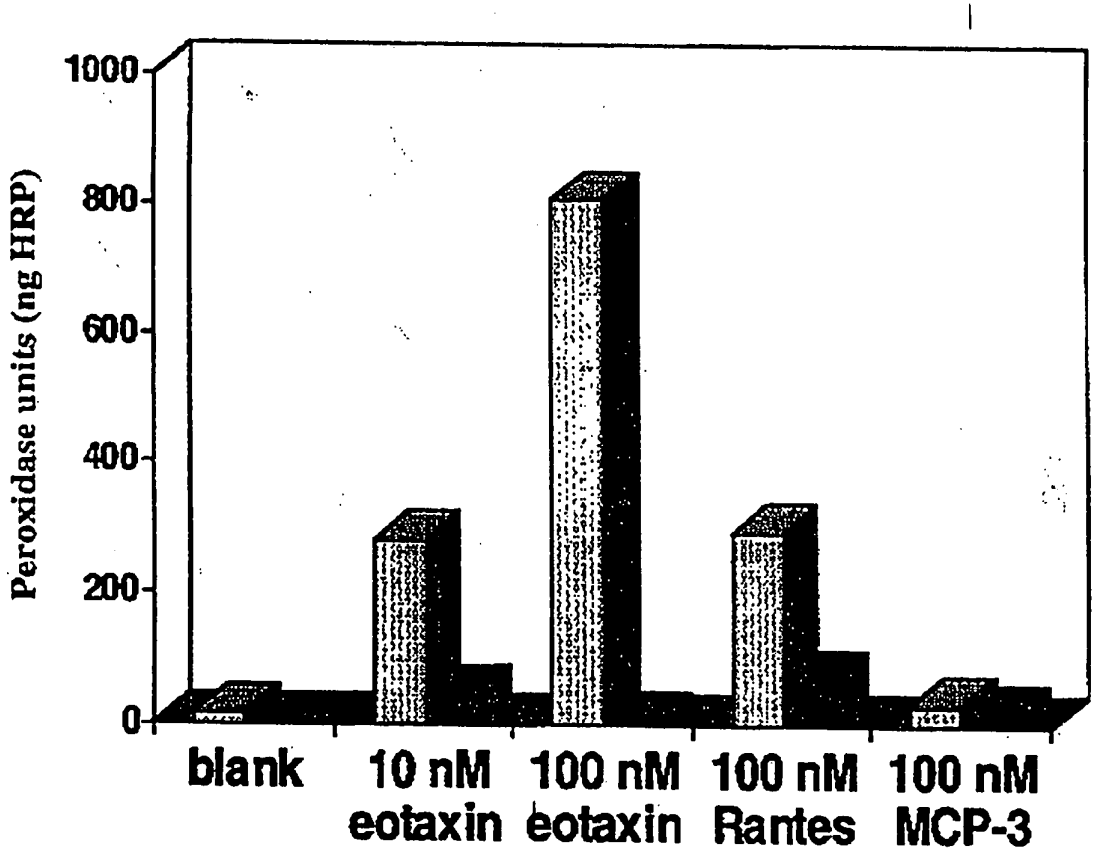
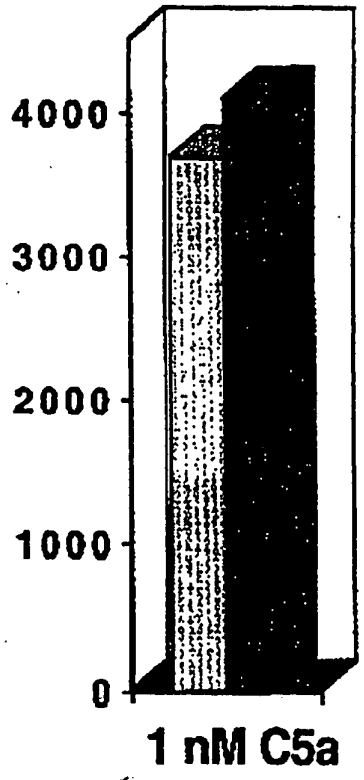


FIGURE 23B



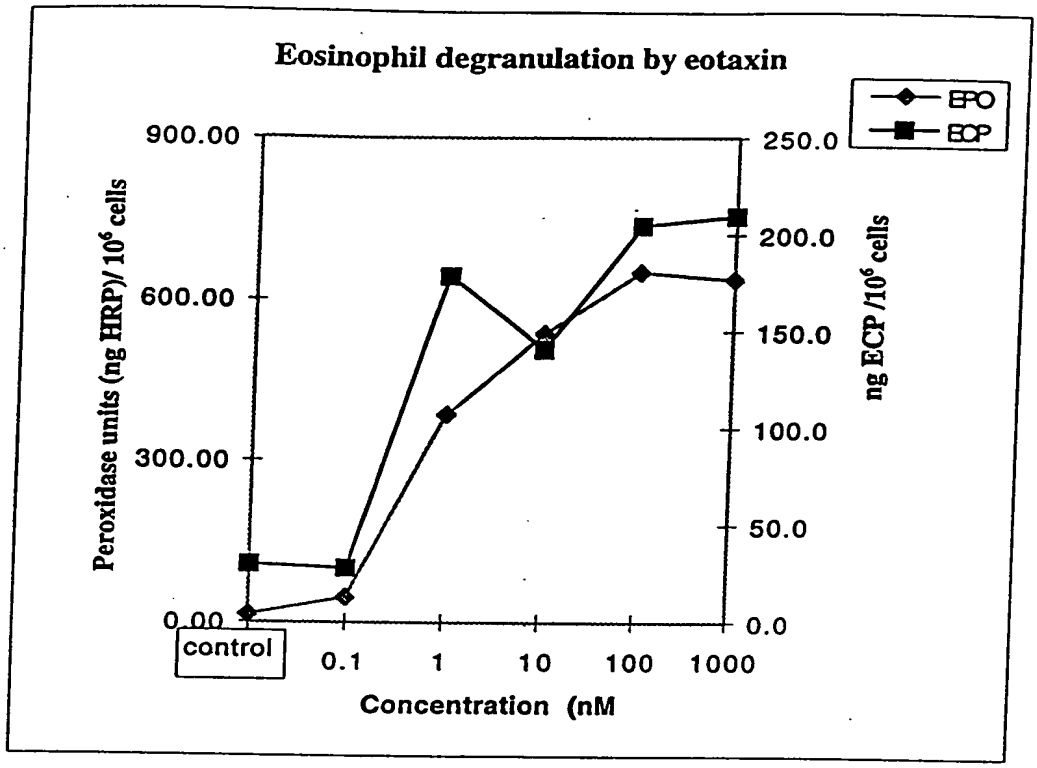


FIGURE 24A

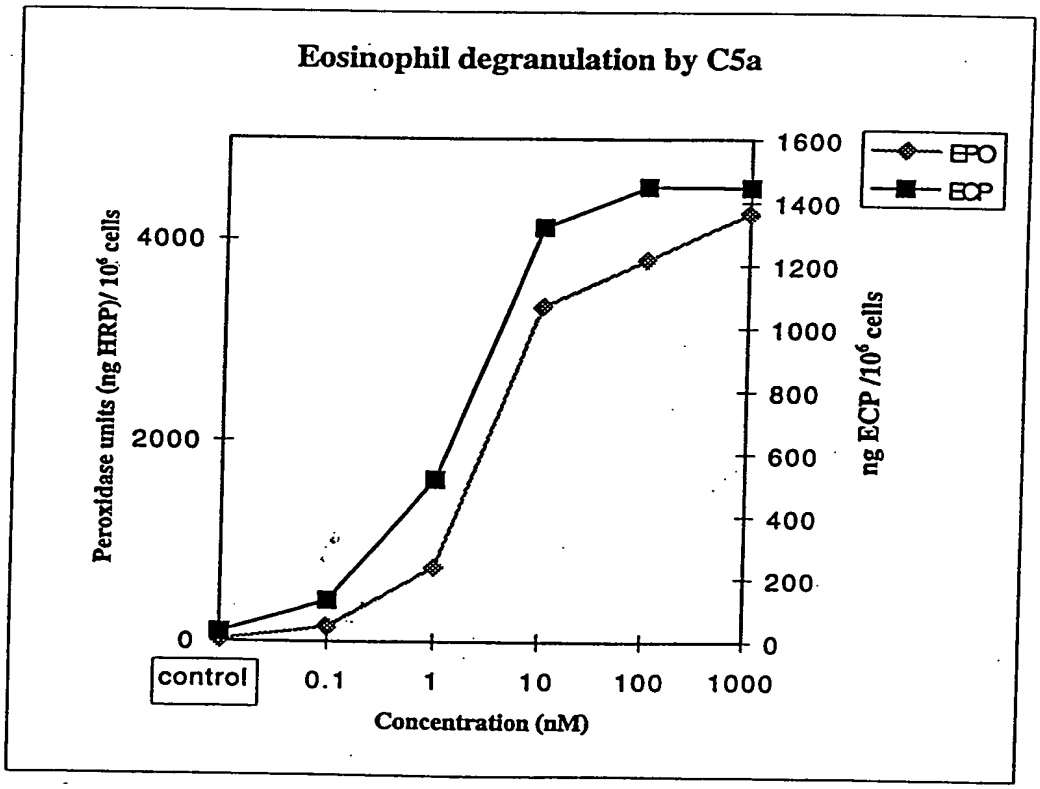


FIGURE 24B

Enzyme release from eosinophil specific granules by eotaxin

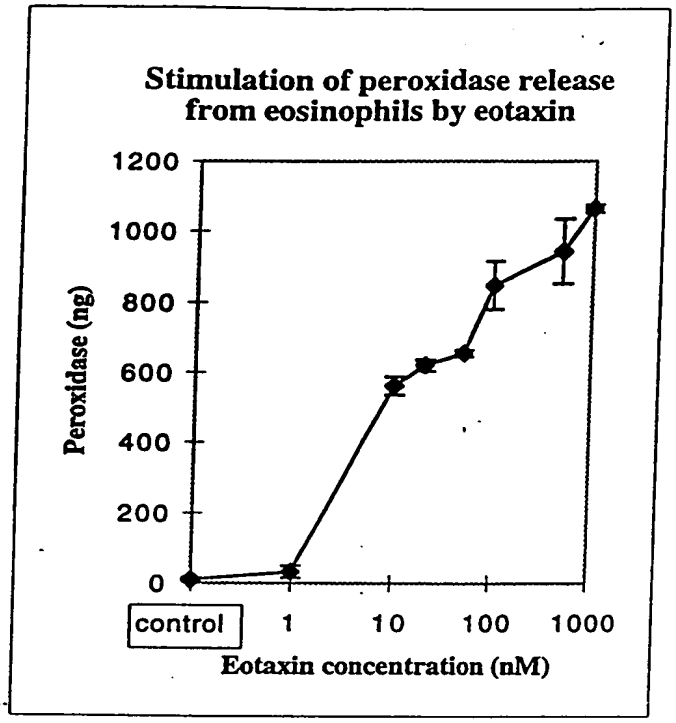


FIGURE 25

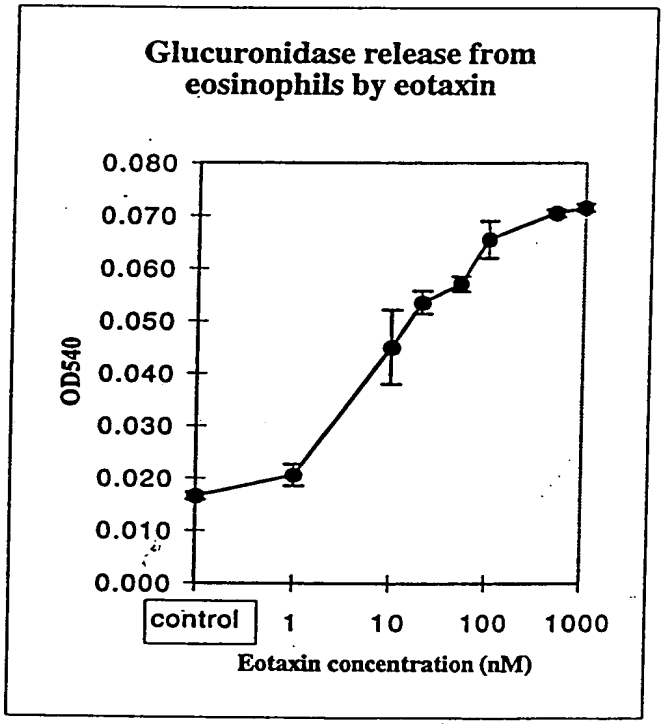


FIGURE 26

Enzyme release from eosinophil small granules by eotaxin

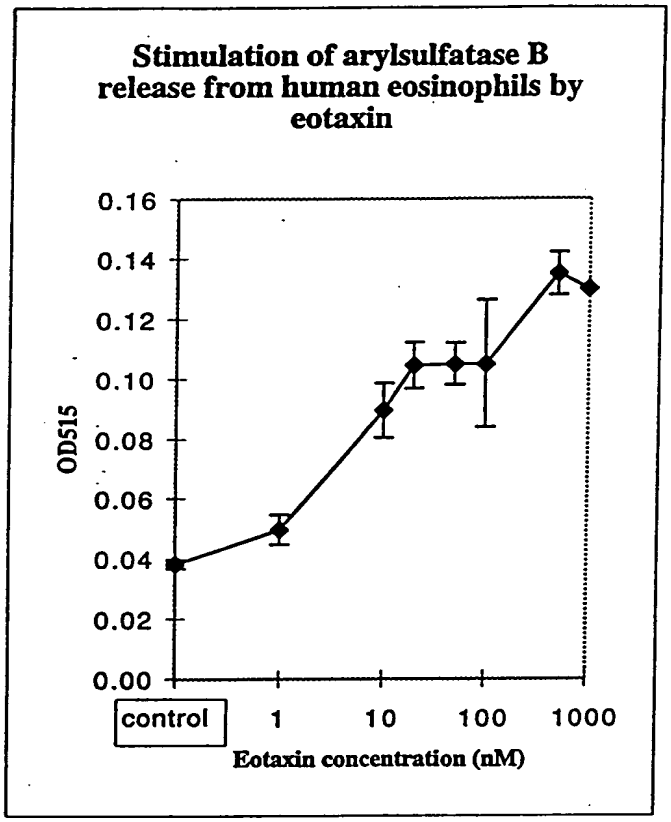


FIGURE 27

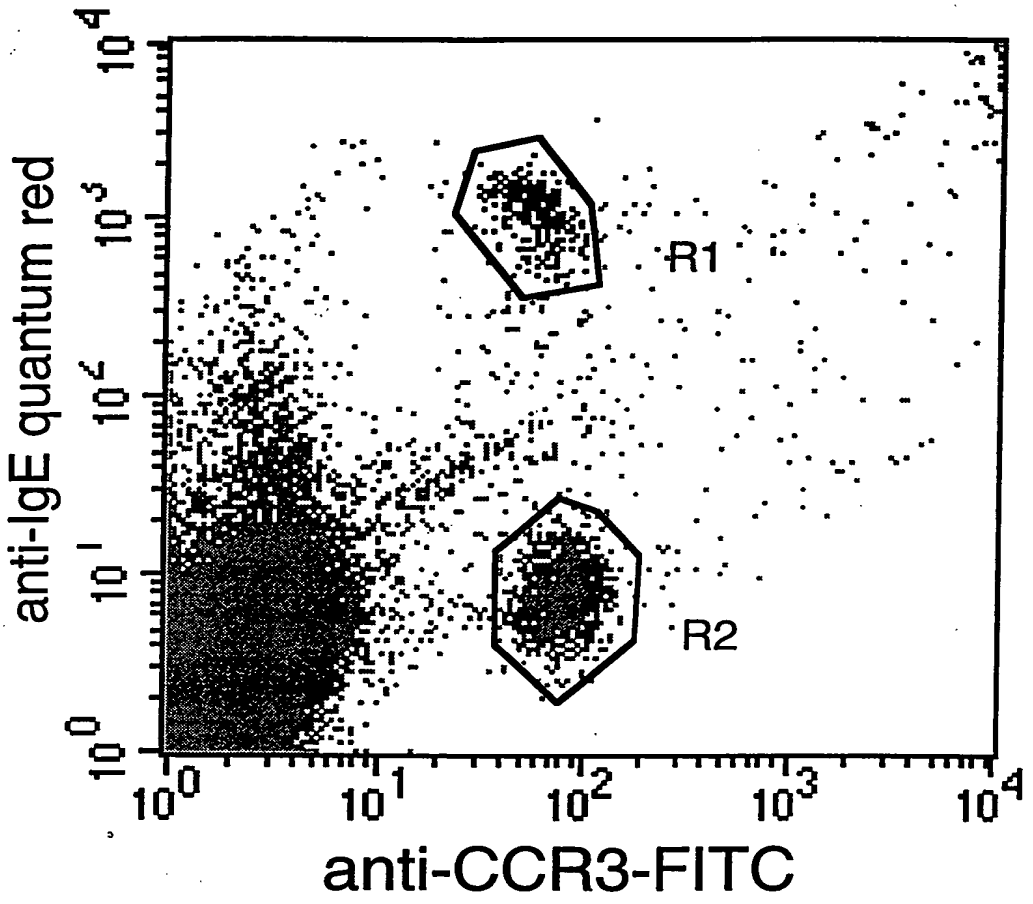


FIGURE 28

Histamine release by human basophils in response to chemokines

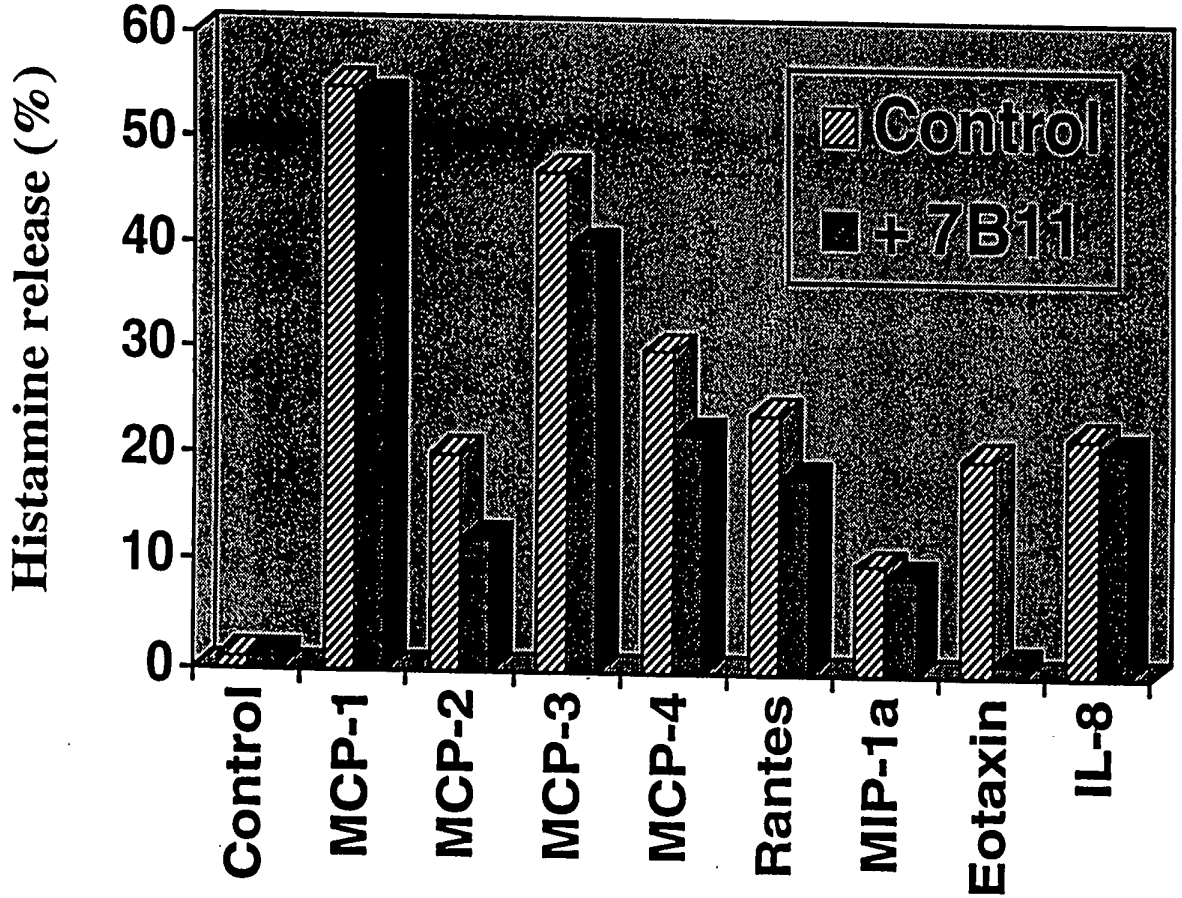


FIGURE 29

Basophils chemotax to eotaxin and MCP-4

Blockade with anti-CCR3 mAb 7B11

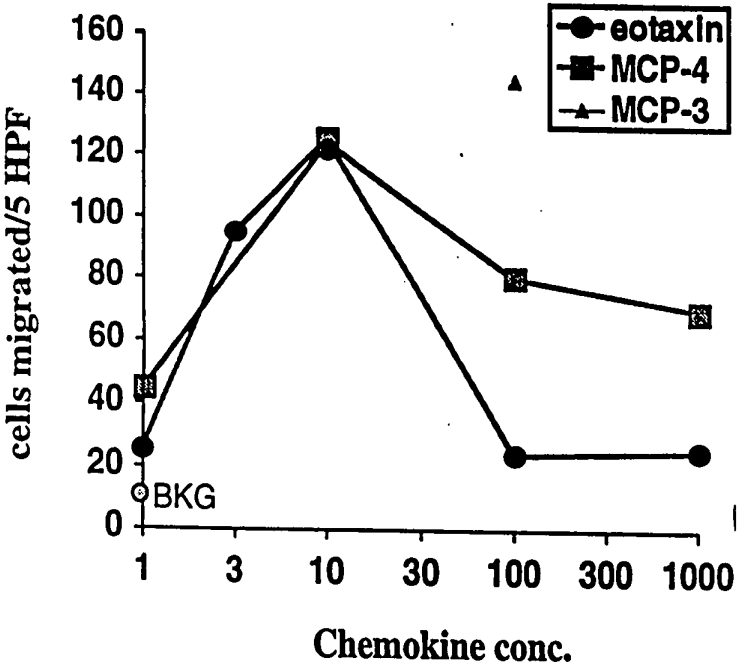


FIGURE 30A

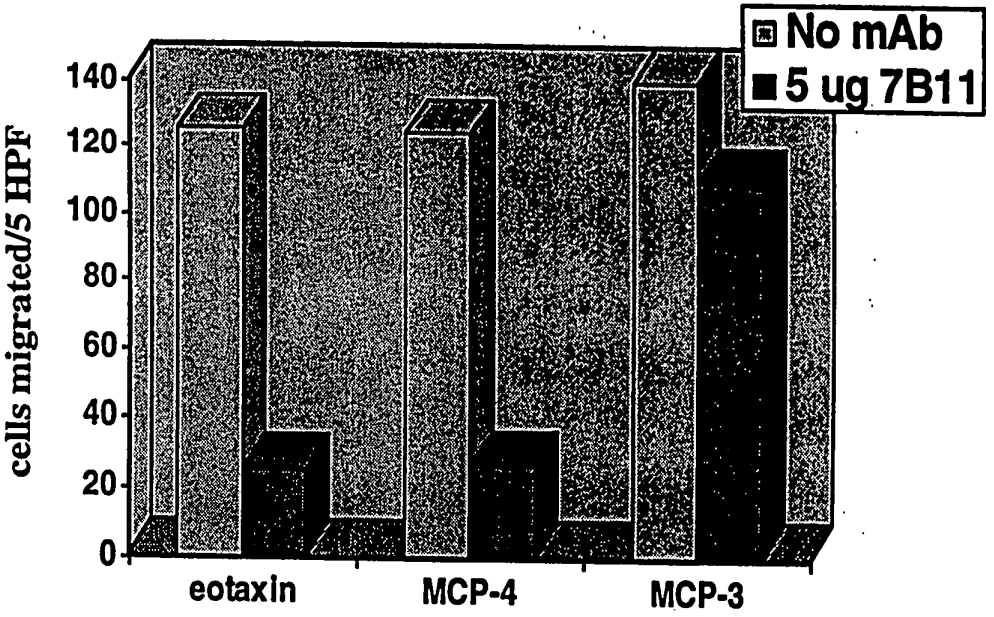


FIGURE 30B